

§Appl. No. 10/009,500
Amdt. dated August 23, 2004
Reply to Office Action of, April 21, 2004

REMARKS

Restriction

SEQ ID NOS. 1, 3, 5, and 7 all code for proteins with manillase (hyaluronidase) properties. See, specification, Page 6, lines 5-7. The attached sequence alignment (Exhibit 1) shows that the amino acid sequences are highly related, sharing at least about 93% identity (about 454/488) between all four isoforms, with high sequence identity between the individual pairs. In a teleconference with Examiner Patterson, it was agreed that Applicant would submit such evidence for his consideration. In view of this submission, it is requested that the restriction between the various forms be withdrawn.

Sequence

The specification has been amended to conform to the sequence rules by adding sequence identifiers to the unidentified sequences. These sequences were already listed in the sequence listing filed February 4, 2003.

Rejection under §101

Claim 20 has been amended to conform with U.S. practice. Support for the amendment can be found throughout the specification, including Page 2, line 27-Page 4, line 9.

Rejections under §112, second paragraph

Claim 16 has been amended to a pharmaceutical composition. Support for the amendment can be found throughout the specification, including Page 6, lines 25-26.

Claims 7, 18, and 19 have been amended to clarify them; these amendments do not change the claim scope, but merely clarify what the skilled worker would have understood from the claim's original wording.

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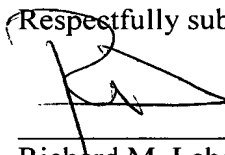
Rejections under §102

It is believed that amendment to claim 18 renders this rejection moot.

In view of the above remarks, favorable reconsideration is courteously requested. If there are any remaining issues which could be expedited by a telephone conference, the Examiner is courteously invited to telephone counsel at the number indicated below.

The Commissioner is hereby authorized to charge any fees associated with this response or credit any overpayment to Deposit Account No. 13-3402.

Respectfully submitted,



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Attorney Docket No.: MERCK-2332

Date: August 23, 2004

EXHIBIT

1

CLUSTAL W (1.82) multiple sequence alignment

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SEQIDNO1.      KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
SEQIDNO7.      KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV  60
SEQIDNO3.      KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
SEQIDNO5.      KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
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                * * *****

SEQIDNO1.      GGTGANWLFDFLDENNKKWDYWAFKDKTPETATITRRWLFRKQNNLKKETEDDLVKLTKG  120
SEQIDNO7.      GGTGANWLFDFLDENNKKWDYWAFKDKTPETATITRRWLFRKQNNLKKETEDDLVKLTKG  120
SEQIDNO3.      GGTGANWLFDFLDENNKKWDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG  120
SEQIDNO5.      GGTGANRLLDFLDENNKKWDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG  120
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                * *****

SEQIDNO1.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO7.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO3.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO5.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
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SEQIDNO3.      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGVGMGVSIVKGLADEAGDHVTAFTL  240
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SEQIDNO7.      HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSTGKD  300
SEQIDNO3.      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSTGTE  300
SEQIDNO5.      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDKPLWLGETSSGYNSTGTE  300
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SEQIDNO1.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWLMLHVHNSLV  360
SEQIDNO7.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWLMLHVHNSLV  360
SEQIDNO3.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWLMLHVHNSLV  360
SEQIDNO5.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYSGYYGPLDKNTLEPNPDYWLMLHVHNSLV  360
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SEQIDNO1.      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIDQYGG  420
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SEQIDNO3.      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG  420
SEQIDNO5.      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIGQYSG  420
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                *****

SEQIDNO1.      KKIYSYILTPEGGQLTSQKVLLNGKELKLVSDQLPELNANESKTSFTLSPKTFGFFVVS  480
SEQIDNO7.      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVS  480
SEQIDNO3.      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVS  480
SEQIDNO5.      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPQLNADESKTSFTLSPKTFGFFVVS  480
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                *****

SEQIDNO1.      ANVEACKK 488
SEQIDNO7.      ANVEACKK 488
SEQIDNO3.      ANVEACKK 488
SEQIDNO5.      ANVEACKK 488
                *****

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CLUSTAL W (1.82) multiple sequence alignment

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SEQIDNO1.      KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
SEQIDNO7.      KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV  60
SEQIDNO3.      KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
SEQIDNO5.      KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
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                *****:*****

SEQIDNO1.      GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETEDDLVKLTKG  120
SEQIDNO7.      GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVLKLTG  120
SEQIDNO3.      GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFNLVLKLTG  120
SEQIDNO5.      GGTFANRLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFNLVLKLTG  120
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                *****:*****

SEQIDNO1.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO7.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO3.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO5.      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNGPDHTS  180
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                *****:*****

SEQIDNO1.      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGVGMGVS YVKGLADGAGDLVTAFTL  240
SEQIDNO7.      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGVGMGVS YVKGLADGAGDLVTAFTL  240
SEQIDNO3.      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGVGMGVSXVKGLADEAGDHVTAFTL  240
SEQIDNO5.      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGVGMGVS YVKGLADEAGDHVTAFTL  240
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                *****:*****

SEQIDNO1.      HQYYFDGNTSDVSTYLDATYFKKLQQLFDKVKDVLKNSQHKDKPLWLGETSSGYNSGTD  300
SEQIDNO7.      HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTD  300
SEQIDNO3.      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED  300
SEQIDNO5.      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDKPLWLGETSSGYNSGTED  300
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                *****:*****

SEQIDNO1.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWL MHVHNSLV  360
SEQIDNO7.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWL MHVHNSLV  360
SEQIDNO3.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWL MHVHNSLV  360
SEQIDNO5.      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYSGYYGPLDKNTLEPNPDYWL MHVHNSLV  360
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                *****:*****

SEQIDNO1.      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGS LTIFALNVGDEEDVTLKIDQYGG  420
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SEQIDNO5.      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGS LTIFALNVGDEEDVTLKIGQYSG  420
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SEQIDNO1.      KKIYSYILTPEGGQLTSQKVLLNGKELKLVSDQLPELNANESKTSFTLSPKTFGFFVVS D  480
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SEQIDNO5.      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPQLNADESKTSFTLSPKTFGFFVVS D  480
                *****
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SEQIDNO1.      ANVEACKK 488
SEQIDNO7.      ANVEACKK 488
SEQIDNO3.      ANVEACKK 488
SEQIDNO5.      ANVEACKK 488
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